

CLAIMS

1. A phytase variant which, when aligned according to Fig. 1, is amended as compared to a model phytase in at least one of the following positions, using the position numbering corresponding to P_lycii:

24; 27; 31; 33; 39; 40; 41; 42; 43; 44; 45; 46; 47; 49; 51; 56; 58;
59; 61; 62; 68; 69; 70; 71; 72; 73; 74; 75; 76; 77; 78; 79; 80; 81;
82; 83; 84; 88; 90; 102; 115; 116; 117; 118; 119; 120; 121; 122; 123;
10 124; 125; 126; 127; 128; 132; 143; 148; 149; 150; 151; 152; 153; 154;
155; 156; 157; 158; 159; 160; 161; 162; 163; 170f; 170g; 171; 172;
173; 184; 185; 186; 187; 187a; 190; 191; 192; 193; 194; 195; 198; 199;
200; 201; 201a; 201b; 201c; 201d; 201e; 201f; 202; 203; 203a; 204;
205; 211; 215; 220; 223; 228; 232; 233; 234; 235; 236; 237; 238; 239;
15 242; 243; 244; 246; 251e; 253; 256; 260; 264; 265; 267; 270; 271; 272;
273; 274; 275; 276; 277; 278; 279; 280; 283; 285; 287; 288; 292; 293;
302; 304; 332; 333; 334; 335; 336; 337; 338; 339; 340; 341; 342; 343;
348; 349; 352; 360; 362; 364; 365; 366; 367; 368; 369; 370; 371; 372;
373; 374; 375; 376; 383k; 387; 393; 394; 396; 404; 409; 411; 412; 413;
20 417; 421; 431.

2. A phytase variant which, when aligned according to Fig. 1, comprises at least one of the following amendments as compared to a model phytase, using the position numbering corresponding to the phytase of P_lycii:

24C; 27P; 31Y; 33C; 39H,S,Q; 40L,N; 42S,G;
43A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 44N; 45D,S; 47Y,F; 49P;
51E,A,R; 56P; 58D,K,A; 59G; 61R; 62V,I; 69Q; 75W,F; 78D,S; 79G; 80K,A;
81A,G,Q,E; 82T; 83A,I,K,R,Q; 84I,Y,Q,V; 88I; 90R,A; 102Y; 115N; 116S;
30 118V,L; 119E; 120L; 122A; 123N,Q,T; 125M,S; 126H,S,V; 127Q,E,N;
128A,S,T; 132F,I,L; 143N; 148V,I; 151A,S; 152G; 153D,Y; 154D,Q,S,G;
157V; 158D,A; 159T; 160A,S; 161T,N; 162N; 163W; 170fH; 170gA; 171N;
172P; 173Q,S; 184Q,S,P; 185S; 186A,E,P; 187A; 187aS; 190A,P; 193S;
194S,T; 195T,V,L; 198A,N,V; 200G,V; 201D,E; 201a(); 201b(); 201c();
35 201d(); 201e(); 201f(); 201eT; 202S,A; 203R,K,S; 203aV,T;
204Q,E,S,A,V; 205E; 211L,V; 215A,P; 220L,N; 223H,D; 228N; 232T; 233E;

235Y,L,T; 236Y,N; 237F; 238L,M; 242P,S; 244D; 246V; 251eE,Q; 253P;
256D; 260A,H; 264R,I; 265A,Q; 267D; 270Y,A,L,G; 271D,N; 273D,K;
275F,Y; 278T,H; 280A,P; 283P; 287A,T; 288L,I,F; 292F,Y; 293A,V;
302R,H; 304P,A; 332F; 336S; 337T,G,Q,S; 338I; 339V,I; 340P,A;
5 343A,S,F,I,L; 348Y; 349P; 352K; 360R; 362P; 364W,F; 365V,L,A,S;
366D,S,V; 367A,K; 368K; 369I,L; 370V; 373A,S; 374S,A; 375H; 376M;
383kQ,E; 387P; 393V; 396R; 404A,G; 409R; 411K,T; 412R; 417E,R; 421F,Y;
431E.

10 3. The phytase variant of claim 1 or 2, which is derived from an
ascomycete phytase.

4. The phytase variant of claim 3, which is derived from an
Aspergillus phytase.

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5. The phytase variant of claim 4, wherein the model phytase is a
strain of *Aspergillus niger*, *Aspergillus ficuum*, *Aspergillus nidulans*,
Aspergillus fumigatus, *Aspergillus terreus*.

20 6. The phytase variant of claim 5 wherein the model phytase is
Aspergillus nidulans DSM 9743; or any of the following strains of
Aspergillus terreus: CBS 116.46, DSM 9076, CBS 220.95.

7. The phytase variant of claim 6 wherein the model phytase is the
25 *Aspergillus nidulans* phytase sequence shown in Fig. 10; or the
Aspergillus terreus phytase sequence shown in Fig. 12.

8. The phytase variant of claim 3 wherein the model phytase is a
strain of *Thermomyces lanuginosus*, *Talaromyces thermophilus*, or
30 *Myceliophthora thermophila*.

9. The phytase variant of claim 8 wherein the model phytase is
Thermomyces lanuginosus CBS 586.94; or any of the following strains of
Talaromyces thermophilus: ATCC 20186, ATCC 74338; or any of the
35 following strains of *Myceliophthora thermophila*: ATCC 34625, ATCC
74340.

10. The phytase variant of claim 9 wherein the model phytase is the *Thermomyces lanuginosus* phytase sequence shown in Fig.14; or the *Talaromyces thermophilus* sequence shown in Fig.13; or the
5 *Myceliophthora thermophila* phytase sequence shown in Fig.7.

11. The phytase variant of claim 3 wherein the model phytase is an ascomycete consensus phytase sequence.

10 12. The phytase variant of claim 1 or 2, which is derived from a basidiomycete phytase.

13. The phytase variant of claim 12, wherein the model phytase is a strain of *Paxillus involutus*, *Trametes pubescens*, *Agrocybe pediades*,
15 or *Peniophora lycii*.

14. The phytase variant of claim 13 wherein the model phytase is *Trametes pubescens* CBS 100232 or *Paxillus involutus* CBS 100231.

20 15. The phytase variant of claim 14 wherein the model phytase is the *Trametes pubescens* phytase sequence of Fig. 4 or either of the *Paxillus involutus* phytase sequences of Figs. 2 and 3.

16. The phytase variant of claim 1 or 2, which comprises at least one
25 of the following amendments:

R24C; V27P; H39Q,S; L40N; G42S;
Q43A,C,D,E,F,G,H,I,K,L,M,N,P,R,S,T,V,W,Y; Y44N; A45D,S; F47Y; S49P;
A51E,R; V56P; A58D,K; V62I; S69Q; Y75W,F; D78S; S79G; K80A; G81A,Q,E;
K82T; K83A,I,R,Q; Y84Q,I,V; E90R,A; D115N; D116S; T118V,L; P119E;
30 F120L; E122A; Q123N,T; L125S,M ; V126H,S; N127Q,E; S128A,T; F132I,L;
I148V; S151A; S153D,Y; S154Q,D,G; I157V; A158D; S159T; G160A,S;
K161T,N; K162N; F163W; R170fH; Q171N; G173Q,S; S184P,Q; E185S;
A186E,P; S187A; T190P,A; P193S; G194S,T; T195V,L; V198A,N; E200G,V;
D201E; S201d(); E201e(),T; L201f(); preferably all three deletions;
35 A202S; D203R,K,S; D203aV,T; V204Q,E,S,A; T211L,V; S215AP; L220N;
D223H; T228N; T235Y,L; Y236N; L237F; M238L; S242P; I246V; K251eE,Q;

H260A; I264R; N265Q,A; Q270Y,A,L,G; S271D,N; K273D; Y275F; H278T;
A280P; T287A; Q288L,I,F; Y292F; A293V; H302R; P304A; N336S; G337S,T,Q;
I339V; S340P,A; F343A,S,F,I,L; N349P; N360R; T362P; F364W; S365V,L,A;
S366D,V; A367K; W368K; T369I,L; A373S: S374A; R375H; L376M; Q383kE;
5 P404A,G; T411K; R417E; F421Y; A431E.

17. The phytase variant of claim 16, the model phytase of which is an *Aspergillus* derived phytase, preferably derived from *Aspergillus ficuum* or *Aspergillus niger*.

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18. The phytase variant of claim 17, the model phytase of which is a phytase derived from either of *Aspergillus ficuum* (niger) NRRL 3135, *Aspergillus niger* ATCC 9142, or *Aspergillus niger* ATCC 74337.

15 19. The phytase variant of claim 18, the model phytase of which is the *Aspergillus ficuum* phytase sequence of Fig. 11.

20. The phytase variant of claim 1 or 2, which comprises at least one of the following amendments:

20 A24C; V27P; H39,S,Q; L40N; G42S; Q43C,D,E,F,H,K,M,P,R,S,W,Y; Y44N;
S45D; F47Y; S49P; E51A,R; L56P; K58D,A; D59G; I62V; S69Q; Y75W,F;
S78D; S79G; K80A; S81A,G,Q,E; K82T; K83A,I,Q,R; Y84Q,V,I; V88K; A90R;
F102Y; D115N; D116S; T118V,L; P119E; F120L; E122A; Q123N,T; L125S,M;
V126H,S; N127Q,E; S128A,T; F132,I,L; S143N; I148V; S151A; S153D,Y;
25 D154Q,S,G; I157V; A158D; S159T; G160A,S; E161T,N; K162N; F163W;
G170fH; ()171N; N173Q,S; T172P; P184Q,S; E185S; S186A,E,P; E187A;
T187aS; T190P,A; G194S,T; V195L,T; K198A,N,V; E200G,V; A201D,E;
S201d(); Q201e(),T; L201f(); preferably all three deletions; G202S,A;
D203R,K,S; E203aV,T; V204Q,E,S,A; A205E; L211V; A220L,N; H223D; T228N;
30 E232T; D233E; V235Y,L,T; V236Y,N; L237F; M238L; C242P,S; T246V;
Q251eE,Q; Q256D; H260A; K264R,I; K265Q,A; N267D; Q270Y,A,L,G; S271D,N;
G273D,K; Y275F; Y278T,H; A280P; A287T; Q288L,I,F; F292Y; T293A,V;
R302H; P304A; F332F; N336S; S337T,G,Q; M338I; V339I; S340P,A;
F343A,S,I,L; N349P; E352K; S360R; K362P; Y364W,F; S365V,L,A;
35 A366D,V,S; S367A,K; W368K; V369I,L; G373S,A; R375H; A376M; K383kQ,E;
D404A,G; K411T; I393V; L412R; K417E,R; W421F,Y; G431E.

21. The phytase variant of claim 20, which is derived from an *Aspergillus* phytase, preferably using a model phytase derived from *Aspergillus fumigatus*.

22. The phytase variant of claim 21, the model phytase of which is a phytase derived from either of the following strains of *Aspergillus fumigatus*: ATCC 13073, ATCC 32722, ATCC 58128, ATCC 26906 or ATCC 32239.

23. The phytase variant of claim 22, the model phytase of which is the *Aspergillus fumigatus* phytase sequence of Fig. 8.

24. The phytase variant of claim 1 or 2, which comprises at least one of the following amendments:

G24C; V27P; H39S,Q; L40N; G42S;
Q43A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; Y44N; S45D; Y47F; S49P;
E51A,R; V56P; D58K,A; D59G; V62I; S69Q; Y75W,F; S78D; S79G; K80A;
S81A,G,Q,E; K82T; A83I,Q,K,R; Y84,Q,I,V; A90R; D115N; D116S; T118V,L;
F119E; P120L; E122A; N123Q,T; M125S; V126H,S; N127Q,E; S128A,T;
Y132F,I,L; K143N; I148V; S151A; S153D,Y; D154Q,S,G; I157V; A158D;
S159T; A160S; E161T,N; K162N; F163W; G170fH; S170gA; Q171N; H173Q,S;
P184Q,S; E185S; G186A,E,P; S187A; G187aS; T190P,A; H193S; G194S,T;
T195V,L; A198N,V; E200G,V; D201E; S201d(); E201e(),T; L201f();
preferably all three; G202S,A; D203R,K,S; D203aV,T; V204Q,S,A,E;
L211V; A215P; L220N; D223H, T228N; E232T; D233E; V235Y,L,T; Y236N;
L237F; M238L; P242S; E244D; E251e,Q; A256D; H260A; R264I; Q265A;
Q270Y,A,L,G; S271D,N; G273D,K; Y275F; Y278T,H; A280P; A287T;
Q288L,I,F; F292Y; A293V; R302H; P304A; N336S; S337T,Q,G; M338I; I339V;
S340P,A; F343A,S,I,L; N349P; A352K; S360R; E362P; Y364W,F; S365V,L,A;
A366D,V,S; S367K,A; W368K; T369I,L; G373S,A; A374S; R375H; A376M;
Q383kE; A404G; K411T; E417R; F421Y; A431E.

25. The phytase variant of claim 24, the model phytase of which is an ascomycete consensus phytase.

26. The phytase variant of claim 25, the model phytase of which is the ascomycetes consensus sequence "conphys" of Fig. 9.

27. The phytase variant of claim 1 or 2, which comprises at least one of the following amendments:

V24C; F27P; ()31Y; F33C; D39H,S,Q; S40L,N; A42S,G;
A43C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; Y44N; T45D,S; Y47F;
Q51E,A,R; K58D,A; K61R; I62V; F75W; S78D; A80K; G81A,Q,E; R83A,I,Q,K;
I84Y,Q,V; V88I; K90R,A; L102Y; D115N; D116S; V118L; P119E; F120L;
10 L123N,T,Q; S125M; S126H,V; Q127E,N; A128S,T; T132F,I,L; E143N; V148I;
S151A; S152G; S153D,Y; N154D,Q,S,G; D158A; S159T; A160S; T161N;
()170fH; ()170gA; ()171N; H173Q,S; H172P; S184Q,P; E185S; S186A,E,P;
L187A; ()187aS; T190P,A; D193S; A194S,T; M195T,V,L; N198A,V; G200V;
S201D,E ()201eT; S202A; D203R,K,S; P203aV,T; Q204E,S,A,V; T205E;
15 I211L,V; P215A; L220N; Q223D,H; A232T; D233E; S235Y,L,T; N236Y; L237F;
I238L,M; A242P,S; E244D; I246V; ()251eE,Q; N256D; P260A,H; A264R,I;
Q265A; E267D; G270Y,A,L; L332F; D271N; D273K; F275Y; T278H; Y280A,P;
Y283P; V287A,T; Q288L,I,F; Y292F; I293A,V; E302R,H; P304A; L332F;
N336S; Q337T,S,G; M338I; I339V; A340P; S343A,F,I,L; F348Y; N349P;
20 S352K; P360R; R362P; W364F; V365L,A,S; T366D,V,S; S367K,A; R368K;
L369I; T370V; S373A; A374S; R375H; S383kQ,E; T387P; A396R; G404A;
L409R; T411K; L412R; E417R; Y421F.

28. The phytase variant of claim 27, the model phytase of which is a phytase derived from *Agrocybe pediades*.

29. The phytase variant of claim 27, the model phytase of which is a phytase derived from *Agrocybe pediades* CBS 900.96.

30. The phytase variant of claim 29, the model phytase of which is the *Agrocybe pediades* phytase sequence of Fig. 5.

31. The phytase variant of claim 1 or 2, which comprises at least one of the following amendments:

F24C; V27P; L31Y; I33C; S39H,Q; N40L; G42S;
P43A,C,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W,Y; Y44N; D45S; F47Y; E51A,R;

E58D,K,A; T61R; V62I; W75F; S78D; A80K; R81Q,E,G,A; S82T; R83A,I,Q,K;
Q84Y,V,I; V88I; K90R,A; A115N; D116S; L118V; P119E; F120L; N123T,Q;
S125M; H126S,V; Q127E,N; T128A,S; M132F,I,L; G143N; V148I; A151S;
D153Y; Q154D,S,G; D158A; S159T; S160A; T161N; ()170fH; ()170gA;
5 S171NG172P; E173Q,S; Q184S,P; E185S; E186A,P; G187A; ()187aS; T190P,A;
N193S; N194S,T; M195T,V,L; N198A,V; V200G; D201E; ()201eT; G202S,A;
D203R,K,S; ()203aV,T; E204Q,S,A,V; S205E; V211L; N215A,P; L220N;
A223D,H; S232T; D233E; L235Y,T; T236Y,N; L237F; M238L; P242S; L246V;
()251eE,Q; A260H; V264R,I; S265Q,A; E267D; Y270A,L,G; D271N; D273K;
10 F275Y; G278T,H; P280A; A283P; T287A; Q288L,I,F; Y292F; V293A; G302R,H;
A304P; N336S; T337Q,S,G; M338I; V339I; P340A; A343S,F,I,L; F348Y;
N349P; A352K; E360R; R362P; W364F; V365L,A,S; D366V,S; S367K,A; L369I;
S373A; G374A,S; ()383kQ,E; E387P; A396R; G404A; V409R; E411K,T; L412R;
E417R; Y421F; A431E.

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32. The phytase variant of claim 31, the model phytase of which is a
phytase derived from *Peniophora lycii*.

33. The phytase variant of claim 32, the model phytase of which is a
20 phytase derived from *Peniophora lycii* CBS 686.96.

34. The phytase variant of claim 33, the model phytase of which is
the *Peniophora lycii* phytase sequence of Fig. 6.

25 35. A phytase polypeptide which comprises a phytase variant according
to any of the previous claims.

36. A DNA construct comprising a DNA sequence encoding a phytase
variant according to any one of claims 1-34.

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37. A recombinant expression vector which comprises a DNA construct
according to claim 36.

38. A host cell which is transformed with a DNA construct according
35 to claim 36 or a vector according to claim 37.

39. A process for preparing a phytase variant, the process comprising culturing the host cell according to claim 38 under conditions permitting the production of the phytase variant, and recovering the phytase from the culture broth.

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40. A feed or food comprising at least one phytase variant of any of claims 1-34.

41. A process for preparing a feed or food according to claim 40,
10 wherein the at least one phytase variant is added to the food or feed components.

42. A composition comprising at least one phytase variant of any of claims 1-34.

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43. The composition according to claim 42 suitable for use in food or feed preparations.

44. The composition of claim 42 or 43, which is an animal feed
20 additive.

45. A process for reducing phytate levels in animal manure comprising feeding an animal with an effective amount of the feed according to claim 40 or obtainable according to claim 41.

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46. Use of the phytase variant of any of claims 1-34; or the composition of claim 42 or 43 for liberating phosphorous from a phytase substrate.

30 47. A transgenic plant or plant part which is capable of expressing a phytase variant of any of claims 1-34.

48. A modified phytase comprising a mutation in an amino acid sequence of a phytase, wherein the modified phytase has phytase
35 activity and the mutation is at one or more positions selected from the group consisting of:

45, 61, 118, 203, 203a, 340, 360, 366, and 411,
wherein each position corresponds to the position of the amino acid
sequence of the mature *P. lycii* phytase (SEQ ID NO: 7).

5 49. The modified phytase of claim 48, wherein the mutation is
selected from the group consisting of:
45D,S; 61R; 118V,L; 203R,K,S; 203aV,T; 340P,A; 360R; 366D,S,V; and
411K,T.

10 50. The modified phytase of claim 48, wherein the phytase is an
ascomycete phytase.

51. The modified phytase of claim 50, wherein the phytase is an
Aspergillus phytase.

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52. The modified phytase of claim 51, wherein the phytase is an
Aspergillus ficuum, *Aspergillus fumigatus*, *Aspergillus nidulans*,
Aspergillus niger, or *Aspergillus terreus* phytase.

20 53. The modified phytase of claim 52, wherein the phytase is an
Aspergillus terreus, CBS 116.46 phytase.

54. The modified phytase of claim 48, wherein the phytase is a
Myceliophthora thermophila, *Talaromyces thermophilus*, or *Thermomyces*
25 *lanuginosus* phytase.

55. The modified phytase of claim 54, wherein the phytase is a
Myceliophthora thermophila, ATCC 34625 or ATCC 74340 phytase.

30 56. The modified phytase of claim 54, wherein the phytase is a
Talaromyces thermophilus, ATCC 20186 or ATCC 74338 phytase.

57. The modified phytase of claim 54, wherein the phytase is a
Thermomyces lanuginosus, NRRL B-21527 phytase.

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58. The modified phytase of claim 48, wherein the phytase is an ascomycete consensus phytase sequence.

59. The modified phytase of claim 48, wherein the phytase is a
5 basidiomycete phytase.

60. The modified phytase of claim 59, wherein the phytase is a *Agrocybe pediades*, *Paxillus involutus*, *Peniophora lycii*, or *Trametes pubescens* phytase.

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61. The modified phytase of claim 60, wherein the phytase is a *Paxillus involutus*, CBS 100231 phytase.

62. The modified phytase of claim 61, wherein the phytase is a
15 *Paxillus involutus*, CBS 100231 Phy-A2 phytase.

61. The modified phytase of claim 60, wherein the phytase is a *Trametes pubescens*, CBS 100232 phytase.

20 64. A feed or food comprising a modified phytase of claim 48.

65. A composition comprising a modified phytase of claim 48.

66. A process for reducing phytate levels in animal manure comprising
25 feeding an animal with an effective amount of the feed of claim 64.

67. A modified phytase comprising a mutation in an amino acid sequence of a phytase, wherein the modified phytase has phytase activity and the mutation is at one or more positions selected from
30 the group consisting of:

24; 27; 31; 33; 39; 40; 41; 42; 46; 49; 56; 59; 68; 69; 70; 71; 72;
73; 74; 75; 76; 77; 78; 81; 82; 84; 116; 117; 119; 120; 121; 122; 123;
124; 125; 127; 128; 132; 149; 150; 151; 152; 155; 156; 157; 158; 159;
160; 161; 162; 163; 170f; 170g; 171; 184; 185; 187; 190; 191; 192;
35 193; 194; 200; 201; 201a; 201b; 201c; 201d; 201f; 202; 223; 228; 232;
233; 235; 236; 237; 239; 243; 246; 253; 256; 271; 272; 274; 275; 276;

277; 279; 280; 283; 285; 287; 288; 292; 293; 304; 332; 333; 334; 335;
336; 338; 341; 342; 343; 348; 349; 362; 364; 367; 368; 369; 370; 371;
372; 374; 375; 376; 387; 393; 394; 396; 409; 412; 413; 421; and 431,
wherein each position corresponds to the position of the amino acid
5 sequence of the mature *P. lycii* phytase (SEQ ID NO: 7).

68. The modified phytase of claim 67, wherein the mutation is
selected from the group consisting of:

24C; 27P; 31Y; 33C; 39H,S,Q; 40L,N; 42S,G; 49P; 56P; 58D,K,A; 59G;
10 69Q; 75W,F; 78D,S; 81A,G,Q,E; 82T; 84I,Y,Q,V; 116S; 119E; 120L; 122A;
123N,Q,T; 125M,S; 127Q,E,N; 128A,S,T; 132F,I,L; 151A,S; 152G; 157V;
158D,A; 159T; 160A,S; 161T,N; 162N; 163W; 170fH; 170gA; 171N;
184Q,S,P; 185S; 187A; 190A,P; 193S; 194S,T; 200G,V; 201D,E; 201a();
201b(); 201c(); 201d(); 201f(); 202S,A; 223H,D; 228N; 232T; 233E;
15 235Y,L,T; 236Y,N; 237F; 246V; 253P; 256D; 271D,N; 275F,Y; 280A,P;
283P; 287A,T; 288L,I,F; 292F,Y; 293A,V; 304P,A; 332F; 336S; 338I;
343A,S,F,I,L; 348Y; 349P; 362P; 364W,F; 367A,K; 368K; 369I,L; 370V;
374S,A; 375H; 376M; 387P; 393V; 396R; 409R; 412R; 421F,Y; and 431E.

20 69. The modified phytase of claim 67, wherein the phytase is an
ascomycete phytase.

70. The modified phytase of claim 69, wherein the phytase is an
Aspergillus phytase.

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71. The modified phytase of claim 70, wherein the phytase is an
Aspergillus ficum, *Aspergillus fumigatus*, *Aspergillus nidulans*,
Aspergillus niger, or *Aspergillus terreus* phytase.

30 72. The modified phytase of claim 71, wherein the phytase is an
Aspergillus terreus, CBS 116.46 phytase.

73. The modified phytase of claim 67, wherein the phytase is a
Myceliophthora thermophila, *Talaromyces thermophilus*, or *Thermomyces*
35 *lanuginosus* phytase.

74. The modified phytase of claim 73, wherein the phytase is a *Myceliophthora thermophila*, ATCC 34625 or ATCC 74340 phytase.

75. The modified phytase of claim 73, wherein the phytase is a *Talaromyces thermophilus*, ATCC 20186 or ATCC 74338 phytase.

76. The modified phytase of claim 73, wherein the phytase is a *Thermomyces lanuginosus*, NRRL B-21527 phytase.

77. The modified phytase of claim 67, wherein the phytase is an ascomycete consensus phytase sequence.

78. The modified phytase of claim 67, wherein the phytase is a basidiomycete phytase.

79. The modified phytase of claim 78, wherein the phytase is a *Agrocybe pediades*, *Paxillus involutus*, *Peniophora lycii*, or *Trametes pubescens* phytase.

80. The modified phytase of claim 79, wherein the phytase is a *Paxillus involutus*, CBS 100231 phytase.

81. The modified phytase of claim 80, wherein the phytase is a *Paxillus involutus*, CBS 100231 Phy-A2 phytase.

82. The modified phytase of claim 79, wherein the phytase is a *Trametes pubescens*, CBS 100232 phytase.

83. A feed or food comprising a modified phytase of claim 67.

84. A composition comprising a modified phytase of claim 67.

85. A process for reducing phytate levels in animal manure comprising feeding an animal with an effective amount of the feed of claim 83.